

Figure 1 (page 1 of 3)

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SEQ ID NO:18 -----
SEQ ID NO:22 TKTSAPFLFTLSLRNMTTEERNVRKTRV-----VDVVDCVIPYIDDPKDRDAVSQVC
SEQ ID NO:20 MGGEAP-----EARRLDRAMSEFGGAGSIPEEALHLVLGYVDDPRDREAVSLVC
SEQ ID NO:37 M-----EDPDIKRCKL--SCVATVDDVIEQVMYITDPKDRDSASLVC
1 60

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SEQ ID NO:18 -----TRPT-----
SEQ ID NO:22 RRWYELDSLTRKHVTIALCYTTTPARLRRRFFPHLESCLKGKPRAAMFNLIPEWGGHVT
SEQ ID NO:20 RRWHRIDALTRKHVTVPFCYAAAPAHLLARFPRLLES LAVKGKPRAAMYGLIPEWGGAYAR
SEQ ID NO:37 RRWFKIDSETREHVTMALCYTATPDRLSRFPNRLRSCLKGKPRAAMFNLIPEWGGYVT
61 120

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SEQ ID NO:18 -----
SEQ ID NO:22 PWVKEISQYFDCLKSLHFRRMIVKSDLQNLARDRGHVHLALKLDKCSGFTTDGLFHIGR
SEQ ID NO:20 PWVAELAAPLECLKALHLRRMVVTTDDDLAALVRARGHMLQELKLDKCSGFSTDALRLVAR
SEQ ID NO:37 PWVTEISNNLRQLKSVHFRRMIVSDLDLDR LAKARADDLETCLKDKCSGFTTDGLLSIVT
121 180

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SEQ ID NO:18 * * * * *
SEQ ID NO:22 --RGLETLFLEESTIDEKENDEWIRELATNSVLETNFFLTDL-RASPEYLTLLVRNCQ
SEQ ID NO:22 FCKSLRVLFLEESSILEKD-GEWLHELALNNTVLETNLFYLTDLAVVKIEDLELLAKNCP
SEQ ID NO:20 SCRSLRTLFLFEECSIADNGT-EWLHDLAVNPNVLETNLFHMTL-TVVVPADLELLAKKCK
SEQ ID NO:37 HCRKIKTLLMEESSFSEKD-GKWLHELALQHTSLEVLNFMTEFAKISPKDLETIARNCR
181 240

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Figure 1 (page 2 of 3)

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* * * * *
SEQ ID NO:18 RLKTLKISECFMPDLVSLFRTAQTLOEFAGGSFEEQGPVASRNYENYFPPSLHRLSLL
SEQ ID NO:22 NLVSVKLTDCIEILDVNFHFKHASALEEFCGGTYNE--E---PERYSAISLPKLCRLGLT
SEQ ID NO:20 SLISLKISDCDFSDLIIGFFRMAASLQEFAGGAFIEQGELT---KYGNVKFSPRLCSLGLT
SEQ ID NO:37 SLVSVKVGDFEILELVGFFKAAANLEEFCCGSLNE--DIGMPEKYMNLVFPKLCRLGLS
241 300

* * * * *
SEQ ID NO:18 YMGTNMQILFPYATAALKKLDLQFTFLSTEDHCQIVQRCNSNLETLEVRDVIGDRGLQVVA
SEQ ID NO:22 YIGKNELPIVFMFAAVLKKLDLLYAMLDTEHCHMLIQRCPNLEVLLETRNVIGDRGLEVLG
SEQ ID NO:20 YMGTNEMPIIFPFSALLKKLDLQYFTLTEDHCHQIAKCPNLLVLAVRNVIGDRGLGVVA
SEQ ID NO:37 YMGPNEMPILFPFAAQIRKLDLLYALLETEHCHTLIQKCPNLEVLLETRNVIGDRGLEVLA
301 360

* * * * *
SEQ ID NO:18 QTCKKLHRLRVERGDDDDQGGLEDEQGRISQVGLMAIAQGCPELTYYWAIHVSDITNAALEA
SEQ ID NO:22 RCCKRLKRLRIERGDDDDQG-MEDEEGTVSHRGLIALSQGCSELEYMAVYVSDITNASLEH
SEQ ID NO:20 DTCKKLQRLRVERGDDDDPG-LQEEQGVSVQGLTTVAVGCRELEYIAAYVSDITNGALES
SEQ ID NO:37 QYCKQLKRLRIERGADDEQG-MEDEEGLVSQGLIALAQGCQCELEYMAVYVSDITNESLES
361 420

* * * * *
SEQ ID NO:18 VGTCSKNLNDFRVLVLLDREAHITELPLDNGVRALLRGCTKLRFFAFYVRPGALSDVGLGY
SEQ ID NO:22 IGTHLKNLCDFRLVLVLLDHEEKITDPLDNGVRALLRGCDKLRFFALYLRGGGLTDVGLGY
SEQ ID NO:20 IGTFCKNLCDFRLVLVLLDREERITDPLDNGVRALLRGCTKLRFFALYLRPGGLSDTGLGY
SEQ ID NO:37 IGTYLKNLCDFRLVLVLLDREERITDPLDNGVRSLLIGCKKLRFFAFYLRQGGGLTDLGLSY
421 480

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Figure 1 (page 3 of 3)

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* * * * *
SEQ ID NO:18 VGEFSKIRYMLLGNVGESDNGIIQLSKGCPSLQKLEVRGC-LFSEHALALAAQLKSLR ***
SEQ ID NO:22 IGQYSPNVRWMLLGYVGESDAGLLEFAKGCPSLQKLEMRGCLFFSERALAVAATQLTSLR
SEQ ID NO:20 IGQYSGIIQYMLLGNVGESDGLIRFALGCENLRKLELRSC-CFSEQALARAIRSMPSLR
SEQ ID NO:37 IGQYSPNVRWMLLGYVGESDEGLMEFSRGCPNLQKLEMRGC-CFSERAIAAAVTKLPCLR 540
481

* * * * *
SEQ ID NO:18 YLWVQGFRRSSPTGTDIMAMVRPFWNIEYIVP-----DQDEPCPEHKRQILAYYSLA *****
SEQ ID NO:22 YLWVQGYGVSPSGRDLVLMARPFWNIELI-PSRKVATNTNPDET VVVEHPAHILAYYSLA
SEQ ID NO:20 YVWVQGYKASKTGHDMLMLMARPFWNIEFTPPSSENANRMREDGEPVCVDSQAQILAYYSLA
SEQ ID NO:37 YLWVQGYRASMTGQDLMQMARPYWNIELI-PSRRVPEVNQQGEIREMEHPAHILAYYSLA 600
541

* * * * *
SEQ ID NO:18 GRRTDCPPSVTLLYPAF----
SEQ ID NO:22 GQRSDFPD TVVPLDTATCVD T
SEQ ID NO:20 GKRSDCPRSVVPLYPA-----
SEQ ID NO:37 GQRTDCPTTVRVLKEPI-----
601 621

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Figure 2 (page 1 of 3)

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***
SEQ ID NO:30 MPVMAPTASL---LLSPRPLPASRRVPSLPA-----LSASGRLLRRARADTRLRVA
SEQ ID NO:32 MALPHSISALATTLTLSSPITKPHKVNPPFSSNRNSQFLTQTRPRSRRLSLTPARVA
SEQ ID NO:36 -----LRVA
SEQ ID NO:38 MRATIPALS---LVTPR-----LPSLAV-----PLAGRLR-EGGRSRTLRLVA
1
60
** * ** ***** ** * ***** *
SEQ ID NO:30 APPSVPGEAD--QAPGETEPSTSSAD--EKFWRDHWYPVSLVEDLDPSVPTPFQLLNR
SEQ ID NO:32 APPSTVEADRLYPEAENNETEEEEFSDESSKFTWRDHWYPVSLIEDLNPLLTPTPFQLLGR
SEQ ID NO:36 APTSVPGAE--RAEEPSTSTSPESSEGEKFWRDHWYPVSLVEDLDPRVPTPFQLLNR
SEQ ID NO:38 APTSVPGEA--EQAEPSTAPES---GEKFSWRDHWYPVSLVEDLDPSRPTPFQLLNR
12
61
* * ** * ***** ** ***** ** * ***** *
SEQ ID NO:30 DLVIWKDPKSGEWVALDDRCPHRLAPLSEGRIDETGCLQCSYHGWSFDGSGACTRIPQAA
SEQ ID NO:32 EIVLWYDKSISQWVAFDDKCPHRLAPLSEGRIDEDGKLCQSYHGWSFDGCGSCVKIPQAS
SEQ ID NO:36 DLVIWNDPNSGDWVALDDRCPHRLAPLSEGRIDETGGLQCSYHGWSFDGSGACTRIPQAA
SEQ ID NO:38 DLVIWKEPKSGEWVALDDRCPHRLAPLSEGRIDETGCLQCSYHGWSFDGSGACTRIPQAM
121
180
***** ** ** * ***** ** ***** ** * ***** *
SEQ ID NO:30 PEGPEAKAVRSPKACAIKFPTLVSQGLLFVWPDENGWKEKATATKPPMLPKFEFDPAFSTV
SEQ ID NO:32 SEGPEARAIGSPKACATRFPTLVSQGLLFVWADENGWKEKAKASNPPMFDDFDKPEFPTV
SEQ ID NO:36 PEGPEARAVRSPRACATKFPTLLSQGLLFVWPDENGWKAKATKPPMLPKFEFDDPAFSTV
SEQ ID NO:38 PEGPEARAVRSPKACAIKFPTLVSQGLLFVWPDENGWKEKAAATKPPMLPKFEFDPAFSTV
181
240

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Figure 2 (page 2 of 3)

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*****
SEQ ID NO:30 TIQRDLYYGYDTLMENVSDPSSHIEFAXHKVTGRRDRARPLPFKMESSGAWGYSNSGNP
SEQ ID NO:32 NIQRDLFYGYDTLMENVSDPSSHIEFAHHKVTGRRDRARPLPFKMDSRGSGWFGSANGNP
SEQ ID NO:36 TIQRDLFYGYDTLMENVSDPSSHIEFAHHKVTGRRDRARPLPFKMESSGAWGYSGANTGNP
SEQ ID NO:38 TIQRDLFYGYDTLMENVSDPSSHIEFAHHKVTGRRDRARPLTFRMESSGAWGYSGANSNP
300
*****
SEQ ID NO:30 RISATFVAPCYALNKIEIDTKLPVVGDKWVIWICSFNIPMAPGKTRSIVCARNFFQFS
SEQ ID NO:32 QISAKFVAPCYMMNKIEIDTKLPVVGDKWVWVICSFNIPMAPGKTRSIVCARNFFQFS
SEQ ID NO:36 RITATFEAPCYALNKIEIDTKLPVVGDKWVIWICSFNIPMAPGKTRSIVCARNFFQFT
SEQ ID NO:38 RITATFEAPCYALNKIEIDTKLPVVGDKWVIWICSFNIPMAPGKTRSIVCARNFFQFT
301
*****
SEQ ID NO:30 MPKAWWQL-----VPRWYEHWTSLNLYDGDMLVLQGEKIFLSAS
SEQ ID NO:32 VPGPAWQVNVILLFAFNKQCIHVTVVPRWYEHWTSLNLYDGDMLVLQGEKIFLSET
SEQ ID NO:36 MPKAWWQF-----VPRWYEHWTSLNLYDGDMLVLQGEKIFLSAS
SEQ ID NO:38 MPKAWWQL-----VPRWYEHWTSLNLYDGDMLVLQGEKIFLAAT
361
*****
SEQ ID NO:30 KESSADINQOYTKITFTPTQADRFVLAFAFWLRKFGNSQPDWFGNPSQEVLPSTVLSKRE
SEQ ID NO:32 KEGG-DINKQYTNITFTPTQADRFVLAFAFWLRKFGNSQPDWFGNSSDQPLPSTVLSKRQ
SEQ ID NO:36 KESSADVNQOYTKITFTPTQADRFVLAFAFWLRKFGNSQPDWYGPSQDALPSTVLSKRE
SEQ ID NO:38 KESSADINQOYTKITFTPTQADRFVLAFAFWLRKFGNSQPDWYGNPTQEALPSTVLSKRE
421
*****

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Figure 2 (page 3 of 3)

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**** ** ***** * ** *** ****
SEQ ID NO:30 MLDRYEQHTLKCSSCKGAYNAFQTLQKVFMGATVA-----VLLLL-----
SEQ ID NO:32 MLDREFEQHTLKCSSCKAAYEGFQTWQKVLIGATVVFCATSGIPSDFQLRVLLAGLAVVSA
SEQ ID NO:36 MLDRYEQHTLKCSSCRGAHKAFTQTLQKVFMGATVVFGATSGIPADVQLRILLGAGALVSA
SEQ ID NO:38 MLDRYEQHTLKCSSCKGAYNAFQTLQKVFMGATVVCCAAAGIPPDVQLRLLIGAAALVSA
481 540

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SEQ ID NO:30
SEQ ID NO:32 AIAFALNQLQKNFEFVDYVVAEID
SEQ ID NO:36 ALAYVFYDRQKHFEFVDYVVAHADID
SEQ ID NO:38 AIAYAFHELOKHFVFVDYVVAHADID
541 564

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